

Craniometric Variation and Homogeneity in Prehistoric/Protohistoric Rapa Nui (Easter Island) Regional Populations

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ABSTRACT Discrete cranial morphological traits of prehistoric/protohistoric Rapa Nui (Easter Island) inhabitants have been examined and have illustrated distinct regional or tribal differences; however, craniometric traits have not been as extensively evaluated to determine if similar regional population differences exist. This study examines the range of variability of Rapa Nui craniometrics and utilizes population genetic techniques to evaluate the level of homogeneity/heterogeneity within the island populations. The data consist of 50 cranio-facial measurements of Rapanui (Easter Islanders) skeletal material from the Late Prehistoric (1680–1722) and Protohistoric (1722–1868) periods. The sample was divided into five tribal regions: North, Northeast, South, Southwest, and West. General linear models (GLM) statistical analyses revealed one variable significant for males and 10 for females across tribal regions, totaling 11 regionally significant variables. Discriminant function analyses utilizing crossvalidation provided classification error rates of 55.8% males and 59.0% for females when utilizing those eleven significant variables. Minimum F_{ST} values for males (0.06378) and females (0.09409) were calculated from unbiased Mahalanobis D^2 values. These values indicate that males have greater between-group homogeneity than females. The determinant ratio for the Northeast tribal region was the only significant ratio, yet all but one of the regional determinant ratios displayed a pattern of greater male than female mobility.

These results indicate that significant craniometric differences between the tribal regions did not exist in prehistoric/protohistoric Rapa Nui populations, supporting the findings of previous research which has documented the homogeneity of the craniometrics of those tribal populations. The calculated minimum F_{ST} values indicate the existence of different levels of heterogeneity between the male and female Rapa Nui regional populations resulting from differential levels of migration and gene flow. This variation reflects the establishment in prehistoric times of extensive tribal marriage *tumus*, and the existence of lineage endogamy/restricted exogamy, not the widespread practice of strict tribal endogamy. *Am J Phys Anthropol* 110:407–419, 1999. © 1999 Wiley-Liss, Inc.

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The existence of two main tribal confederacies on prehistoric/prohistoric Rapa Nui (Easter Island), the *Tu'u* and *Hotu'iti*, was reported by Métraux (1940), and the tribes within them are known to have occupied distinctly separate areas (McCoy, 1973; Métraux, 1940; Routledge, 1919). Cultural and ethnographic information, primarily oral histories, has been the primary basis for the ascertainment of tribal and confederacy existence and has been the source for ethnohistoric interpretation of tribal differences on Rapa Nui. The degree to which these tribal groups can be differentiated may be a function of cultural and genetic isolation and/or flow, endogamy, and exogamy. Statements by Métraux (1940, 1957) regarding the practice of tribal endogamy with limited intertribal exogamy on prehistoric Rapa Nui, especially among members of the aristocratic *Miru* tribe of the north and northwest coast, have been supported recently by the osteological examination of regional cranial and postcranial discrete trait frequencies (Chapman and Gill, 1997; Gill et al., 1997). Additionally, distinct patterns of directional gene flow and postmarital residence have been demonstrated by the studies of Zimple and Gill (1986), Chapman (1993), and Gill and Owsley (1993). These studies indicate that the *Miru* tribe practiced strict endogamy, and that when a *Miru* married outside of the tribe, predominantly with south coast tribes, that particular individual moved out of the *Miru* tribal area. The occurrence of limited exogamy between tribes of the northeast and south coasts is also indicated by these studies. The locations of the ancient tribal boundaries depicted by Routledge (1919) assisted in explaining the discriminant function and discrete trait frequency analysis results obtained.

Despite the considerable number of discrete cranial morphological studies of the prehistoric and protohistoric tribes of Rapa Nui, craniometric traits have not been as extensively evaluated to determine if similar regional tribal differences exist and if similar patterns of gene flow are demonstrated (Baker et al., 1997; Kelly et al., 1986; Stefan et al., 1998). Instead, preliminary craniometric analyses have concentrated on addressing the issues concerned with the

Polynesian origins of the prehistoric Rapanui (Easter Islanders) or have evaluated their similarities to other Polynesian populations (Baker and Gill, 1997; Brace et al., 1990; Brace and Hunt, 1990; Gill, 1986; Gill and Owsley, 1993; Gill et al., 1983; Howells, 1990; Murrill, 1968; Owsley et al., 1994; Pietrusewsky, 1990a,b). Dental metrics and nonmetrics have also been utilized to assess the relationships of the Rapanui to other Polynesian populations (Swindler et al., 1998; Turner and Scott, 1977). This study has four objectives: 1) examine the range of craniometric variability of Rapa Nui tribal groups and determine whether various craniometric variables can be utilized to discriminate regional tribal populations; 2) determine if patterns of tribal relationships are observed utilizing craniometric traits, i.e., patterns which correspond with those observed in discrete traits; 3) assess patterns of male and female variation to determine mobility patterns; and 4) determine if craniometric data support the theory of tribal endogamy (Métraux, 1940).

Materials

Craniometric data were collected on 334 late prehistoric/protohistoric Rapanui crania from collections in Rapa Nui, North and South America, and Europe. The craniometric data collected by the author were from the collections curated at the Musée de l'Homme and the Institut de Paléontologie Humaine, Paris, the Natural History Museum, London, the Anthropologische Abteilung, Naturhistorisches Museum, Vienna, the American Museum of Natural History, New York, and the Smithsonian Institution, Washington, DC. During the 1981 Easter Island Anthropological Expedition and subsequent field laboratory sessions between 1981–1991, Dr. George W. Gill, Dr. Douglas W. Owsley, and anthropology graduate students from the University of Wyoming collected and kindly provided additional osteometric data from collections on Rapa Nui and in North and South American museums. Of those 334 crania, only 205 have sufficient provenience information to determine the region of Rapa Nui from which they were collected (Table 1). Comparisons between five tribal region samples

and between male/female samples were conducted on 50 craniometric variables (see Appendix) (Bass, 1995; Gill, 1971; Gill et al., 1988; Howells, 1973).

In order to utilize the Rapanui data collected by Gill and others, interobserver error rates were calculated. Throughout the collection of Rapanui data during Easter Island Anthropological Expedition and subsequent field laboratory sessions, Gill conducted interobserver error assessments between himself, Owsley, and other individuals collecting metric data and found no significant interobserver errors (Gill, personal communication). To assess interobserver error between the author and Gill, a sample of 28 Marquesas and 2 Rapanui crania were measured. Interobserver error rates were tested via pairwise *t*-tests across all variables. A Bonferroni and a Dunn-Sidak method for calculating the experimentwise error rate for multiple comparisons was utilized to determine the significance levels of each comparison (Šidák, 1967; Ury, 1976).

The chances of committing a type I error (rejecting a null hypothesis that is correct) increase with the number of tests performed. In order to minimize the chance of committing a type I error, an experimentwise error rate, $\alpha' = 1 - (1 - \alpha)^{1/k}$ was calculated, where α is the desired experimentwise error rate and k is the number of pairwise comparisons to be made. The experimentwise error rate lowers the probability of making a type I error for each comparison, so that the probability of making any type I error in the entire series of tests does not exceed α (Sokal and Rohlf, 1995). To maintain an experimentwise error rate of $\alpha = 0.05$, with 50 variable comparisons being conducted, each comparison was determined to be significant only if the observed *P*-value for the *t*-test was less than the $\alpha' = 0.001$ level.

The Rapanui skeletal materials were recovered from sites located throughout the island and were separated into regions according to tribal boundaries described in the ethnographic literature (Métraux, 1940; Routledge, 1919). The five regions have been designated as the North Coast (*Ahu Nau Nau*, Anakena beach and other North Coast sites), Northeast (*Ahu Heki'i*, La Pérouse

Bay and *Mahatua* sites), South Coast (*Akahanga* sites, *O'nero*, *Ana Mahiha*, *Koe Hoko*, *Oroi* caves, *Ahu One Makihi*, and *Tongariki* sites), Southwest (*Vaihu* and *Vinapu*), and West Coast (*Ana Kai Tangata*, *Ana Tepahu*, *Ahu Kihikihi Rau Me'a*, *Tahai*, *Tautira*, *Tepeu*, and *Ko Te Riku*) (Chapman and Gill, 1997) (Fig. 1). Stevenson (1981, 1983) has obtained obsidian hydration dates for the Rapanui skeletal material ranging from the Late Prehistoric (A.D. 1680–1722) to the Protohistoric (A.D. 1722–1868). A recent study examined these Rapanui skeletal museum collections, collections dated to these time periods, and determined that there were no significant differences between the collections, indicating that excessive variation has not accumulated due to temporal trends or gene flow within a given collection (Stefan, 2000). There were no apparent temporal changes of the Rapanui crania through the Late Prehistoric and Protohistoric periods, changes that would prevent the utilization and pooling of those samples or complicate their analyses.

The sex of individuals was assessed utilizing pelvic morphology when available. However, most sex assessments were based on cranial morphology and were supplemented by discriminant function analysis assignments (Giles and Elliot, 1962). Individuals were recorded as male, female, possible male, possible female, or indeterminate upon anthroposcopic evaluation. Individuals assigned as a probable male or female were definitively recorded as male or female if discriminant function analysis further supported the anthroposcopic assessment. The sample of crania utilized in this study included only those individuals that could be confidently classified as male or female. Additionally, individuals with unknown site or tribal region provenience information were removed from the sample.

Statistical Methods

A general linear model (GLM) for unbalanced analysis of variance (ANOVA) method of analysis was conducted on each variable to determine if significant tribal differences exist within the male and female sample. An unbalanced analysis was required due to the unequal sample sizes of the five tribal re-

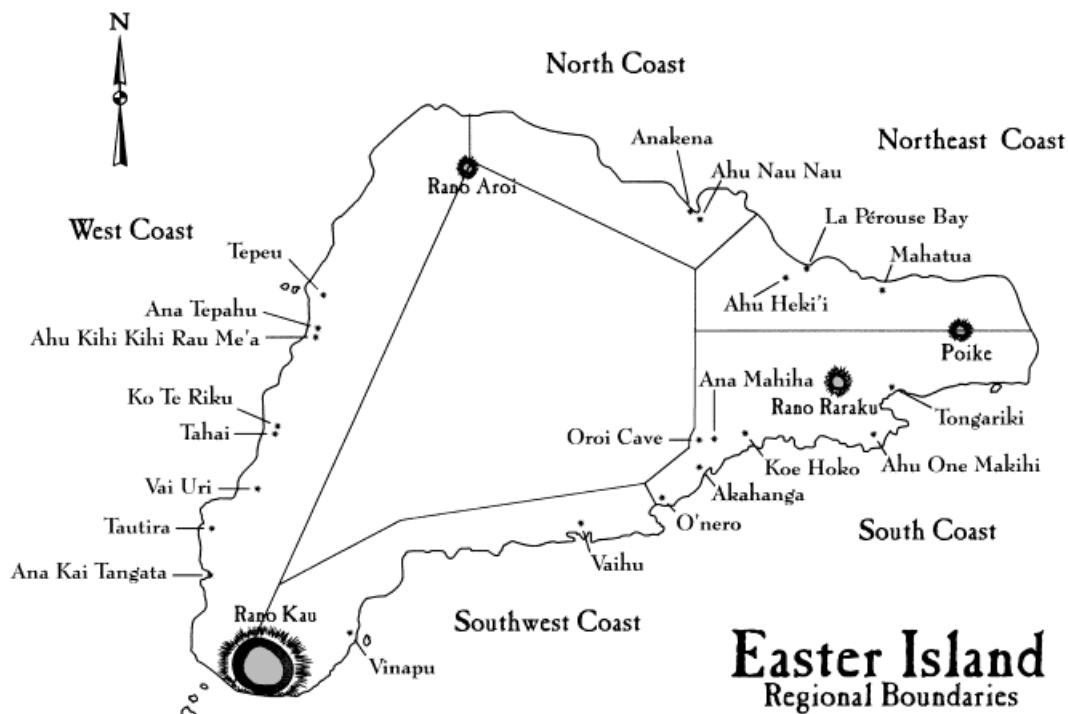


Fig. 1. Rapa Nui regional boundaries and sample site map (adapted from Métraux, 1940, p 8).

gions (Table 1). In order to utilize all significant variables, as well as all five regional samples, the analyses were conducted on two distinct combinations of variables and regions. Analyses were conducted utilizing all regionally significant variables with only the Northeast, South, Southwest, and West regional samples included, and on six regionally significant variables with all five regional samples included.

Due to the small sample sizes of some of the regional Rapanui populations, statistical methods designed for estimating missing variable values could not be utilized. Other approaches to estimating missing values were tried, but these methods have potential problems: they require the number of observations to exceed the number of variables to be estimated, in order to perform certain prediction and matrix operations. Methods which utilize regression predictions can compound sampling error when missing data are predicted for small groups and when relatively few complete observations are available for generating the predic-

tion equations (Droessler, 1981). The option of utilizing a pooled group sample for generating prediction equations was not considered to be viable because the prediction for the smaller groups would be biased toward the larger groups, and the uniqueness of the smaller groups would be lost. Therefore, to maximize the number of observations in each regional sample, to utilize all significant variables, and to maintain group distinctiveness, sex-specific regional means were substituted for missing variables. By utilizing group variable means for missing values, intragroup variation will tend to decrease while intergroup variation will increase. This increase in intergroup variation will artificially increase regional differences and discrimination (Droessler, 1981). The use of group means will also artificially inflate "endogamy," while the use of a grand mean would inflate "exogamy." The utilization of group means is a conservative method, in that it should be harder to reject the null hypothesis of endogamy. As a consequence, the results obtained from the discriminant

function analyses, the calculated minimum F_{ST} values, and the determinate ratio values need to be assessed with caution.

Discriminant function analyses were conducted on the significantly different craniometric variable combinations for males and females in order to provide a more complete assessment of the degree of overlap in the range of variation between tribal regions. Discriminant analysis is frequently done using resubstitution. However, this approach potentially biases the results when sample sizes are small, since the discriminant function utilized to classify each specimen already contains the variation introduced by that specimen. Therefore, discriminant function analyses were carried out using jackknifing. This approach sequentially removes each individual and recalculates the discriminant function based on the remaining specimens. The removed individual is then evaluated by the corresponding function. Classification accuracy typically decreases when the individual being evaluated is excluded from the data set producing the discriminant function. Yet, given the goals of evaluating the degree of distinctiveness of the five tribal regions, this more conservative approach is preferable.

Discriminant function analyses also generate Mahalanobis generalized squared distances (D^2) values that represent the mathematical distances between the centroids of all possible population pairings. These values are biased estimators, for they rely on samples to estimate population parameters (van Vark and Schaafsma, 1992). Subtracting a bias correction value from the corresponding generalized distance value produces unbiased estimators of D^2 . These values adjust for biases introduced by small sample sizes, different sample sizes between comparison pairs, and the number of variables utilized in the analysis (Magnus and Neudecker, 1988; Relethford, 1991; Relethford et al., 1997). Konigsberg et al. (1994) demonstrated the necessity of utilizing a bias correction factor when conducting analyses on small sample sizes. F -statistics are calculated for each unbiased D^2 value to indicate their statistical significance (Droessler, 1981). The resulting unbiased D^2 values are then assessed and utilized to

calculate a minimum F_{ST} value (Konigsberg and Blangero, 1993; Relethford, 1991; Relethford and Blangero, 1990; Williams-Blangero and Blangero, 1989). Minimum F_{ST} values are a minimum estimation of the degree of similarity/dissimilarity of the subgroups within the total population. Unbiased D^2 and minimum F_{ST} values were calculated for males and females utilizing all significant variables, via a program discussed in Relethford et al. (1997) which utilizes a standard bias correction for sampling bias due to small sample sizes (Relethford, 1991) and a heritability factor. An assumption of equal population sizes was incorporated due to the lack of ethnographic or demographic information dealing with prehistoric tribal population sizes.

Minimum F_{ST} values are typically an estimate of the population F_{ST} made under the assumption of complete heritability of the traits being investigated, with no environmental effects on the traits. However, the actual value of F_{ST} is dependent on heritability. Devor (1987) reported average heritabilities for craniometric dimensions from four populations based on path analysis, with the average heritabilities ranging from 0.45–0.60 across those populations and an overall average of 0.55 (Relethford, 1994; Relethford and Harpending, 1994). Donnelly et al. (1998) similarly utilized an average heritability of eight craniometric variables of 0.55 in their analyses of Neandertal and early modern humans. This study will therefore use a heritability value of 0.55 for the calculation of unbiased D^2 and minimum F_{ST} values.

In order to determine if the patterns of regional similarity/dissimilarity could be explained via postmarital residence migration (patrilocal/matrilocal, endogamy/exogamy), within-region variances for the male and female samples were considered to evaluate the mobility of each sex (Konigsberg, 1988). Green (1976) found that the determinate of the covariance matrix between traits could be utilized as a generalized variance measure. The covariance matrices were formed separately by region and sex, ultimately producing a male, $|C\delta|$, and female, $|C\varphi|$, determinate for each region. In order to calculate a nonzero determinate, the covari-

ance matrix must not be singular (Manly, 1994). A singular covariance matrix will be produced if the number of variables is equal to or greater than the number of observations. Due to this limitation and the fact that the North region female sample contained seven individuals, the number of regionally significant variables utilized had to be reduced to six in order to have all regions represented in the analyses. When all significant variables were utilized, the North region samples had to be removed from the determinate analyses.

The ratio of the male determinate to female determinate, $|C\delta|/|C\phi|$, was then utilized to compare the level of male and female within-region variation (Konigsberg, 1988). This ratio implies that within individual regions, with males and females having equal mobility, the ratio of male to female variances should equal one, exceed one if the males were more mobile, or be less than one if females were more mobile. The greater the mobility, the greater the migration into and out of the region, thereby producing increased variability.

A Monte Carlo randomization procedure was utilized to calculate significance levels for the determinate ratios. The observed male/female determinate ratios were compared to the distribution of ratios obtained via 1,000 random permutations of the original regional data set in order to provide a *P*-value to three decimal places. In each randomized permutation of the pooled male/female data set, the male/female subsample sizes were fixed equal to the actual number of males and females in the original regional sample. The significance level (*P*-value) of each determinate ratio is the percentage of the randomized ratios greater than or equal to the observed ratio. All of the statistical analyses were performed on SAS (version 6.12; Cary, NC).

Results

Interobserver error

The results of the interobserver error analyses indicate that four variables are significantly different between the data collected by the researcher and those collected by Gill ($\alpha' \leq 0.001$): porion-bregma $P = 0.001$, porion-subspinale $P < 0.001$, porion-

TABLE 1. Regional samples

Region	Male (n)	Female (n)
North	12	7
Northeast	36	27
South	31	21
Southwest	23	17
West	19	12

prosthion $P < 0.001$, and maxillofrontal subtense $P < 0.001$. Despite their significance, however, the mean differences between the data are no greater than ± 1 mm (porion-bregma, -0.57 mm; porion-subspinale, -0.48 mm; porion-prosthion, -0.70 mm; maxillofrontal subtense, 0.37 mm). Due to this fact, it is not unreasonable to pool the data collected by this researcher and those of Gill et al.

GLM analyses

Table 2 contains the measurements found to be significant between regions for the male and female samples and their associated *P*-values. It is apparent that the prehistoric Rapanui females are craniometrically more variable than the males. The 11 measurements found to be regionally significant are representative of cranial breadth (maximum cranial breadth, maximum frontal breadth, minimum cranial breadth, biasterionic breadth), facial breadth (orbital breadth-dacryon, biorbital breadth), facial height (nasion-alveolare), facial projection and prognathism (porion-subnasale, porion-prosthion, alpha subtense), and mastoid breadth.

As was discussed previously, two combinations of variables and regional samples were necessary. In order to utilize all 11 regionally significant variables, only the Northeast, South, Southwest, and West regional samples could be incorporated due to their sufficiently large sample sizes. However, in order to incorporate all the regional samples, the number of variables utilized had to be reduced to six to facilitate covariance matrix determinate calculation (maximum frontal breadth, biasterionic breadth, orbital breadth-dacryon, minimum cranial breadth, porion-prosthion, alpha subtense). These six variables were chosen due to their high level of significance in the regional female samples. The results of the additional analy-

ses will be referenced in terms of either an "11-variable" or "six-variable" analysis.

Discriminant analysis

The discriminant analyses with crossvalidation provide significantly high levels of misclassification if the specimens are considered as deriving from the five tribal regions. The discriminant analyses for the male sample provide a total classification error rate of 55.8% (with crossvalidation), and the female sample provides a total classification error rate of 59.0% (with crossvalidation) when all 11 significant variables are utilized, and 59.0% and 65.7%, respectively, when the six significant variables are utilized. Table 3 contains the unbiased Mahalanobis generalized squared distance (D^2) values calculated by the male and female sample discriminant analyses, and the minimum F_{ST} values calculated from the unbiased D^2 values. The female sample appears more regionally distinctive than the male sample; however, no male or female D^2 values are significant at the $\alpha = 0.05$ level (Table 4).

Determinant ratio analysis

Table 5 contains the observed ratios of the determinants, $|C\delta|/|C\eta|$, of the male within-group covariance matrixes to the determinants of the female covariance matrices. Four of the five regions have observed determinant ratios that were greater than one with the six-variable analysis, with the Northeast region possessing an extremely large ratio, while the North region possesses a moderately large ratio. These values indicate an overall pattern of increased male mobility within the prehistoric Rapa Nui regional samples. However, the randomization probabilities indicate only one significant departure from a determinant ratio of one at the $\alpha = 0.05$ level, the Northeast region. Though large, the determinate ratio for the North region is not significant and may be an artifact of the small sample sizes or an undetermined sampling bias. Konisberg (1988) also obtained large determinant ratios that were not significant.

The determinant ratios obtained from the 11-variable analyses are obviously quite large. However, only the determinant ratio for the Northeast region is significant at the

$\alpha = 0.05$ level. The determinant ratio for the West region is extremely large, yet not statistically significant. The cause of this large ratio is the small determinant of the female covariance matrix, which may be a function of sampling bias and low power for these values of n . The finding that there was potential tribal exogamy, with greater male postmarital mobility, supports the rejection of the null hypothesis of tribal endogamy, even with the group mean substitution method employed to handle missing data.

Discussion

The regional distinctiveness of prehistoric Rapa Nui islanders, with regards to cranial and postcranial discrete traits, have been investigated and documented by past research (Chapman and Gill, 1997; Chapman, 1993; Gill et al., 1997; Zimple and Gill, 1986), with the results being utilized to support certain ethnographic accounts of tribal endogamy and/or limited exogamy (Métraux, 1940, 1957; Routledge, 1919), particularly for the *Miru* tribe. The distinct frequency patterns of the discrete traits analyzed (i.e., bipartite patella (*Ahu Nau Nau*, North coast); supracondylar foramen of the humerus (*Ahu Kihiki Kihiki Rau Me'a*, West coast); ankylosed sacroiliac joints (*Oroi* cave, South coast)), suggest that limited gene flow occurred between the various regional tribes (Gill et al., 1983). Zimple and Gill (1986) and Baker et al. (1997) have also indicated the presence of bidirectional gene flow between the South and Northeast coasts and unidirectional gene flow from the North coast to the South coast, utilizing cranial discrete trait frequencies and craniometrics. A cursory analysis of only eight craniometric measures, however, reveals a relatively homogeneous prehistoric Rapa Nui population (Kelly et al., 1986).

Stefan et al. (1998) documented considerable sexual dimorphism within the Rapa Nui islanders. Yet, of the 50 craniofacial measurements analyzed, only one was regionally significant for males, and 11 were regionally significant for females (Table 2). The high level of male homogeneity is further indicated by the high classification error rates of the discriminant function analyses performed. The conservative nature of

TABLE 2. General linear models analysis results of regionally significant craniometric measurements for males and females

Variable	Male <i>P</i> -value	Female <i>P</i> -value
Maximum cranial breadth	0.1851	0.0360
Maximum frontal breadth ¹	0.4394	0.0218
Nasion-alveolare	0.1942	0.0404
Biasterionic breadth ¹	0.0539	0.0241
Left orbital breadth-dacryon ¹	0.0739	0.0003
Biorbital breadth	0.1268	0.0261
Minimum cranial breadth ¹	0.1374	0.0074
Porion-subnasale	0.7415	0.0393
Porion-prosthion ¹	0.1416	0.0125
Alpha subtense ¹	0.4731	0.0206
Mastoid breadth	0.0042	0.5368

¹ Variables utilized in six-variable analyses.

the crossvalidation technique typically increases the classification error rates, yet it ensures that realistic expectations of population discrimination are obtained. Despite the inability to accurately discriminate the Rapa Nui tribal region populations, the unbiased Mahalanobis D^2 values (Table 3) indicate differing levels of homogeneity/heterogeneity for males and females. Regionally, females appear to have been more distinctive across groups than males. However, as with the males, no female unbiased D^2 values were significant at the $\alpha = 0.05$ level, further indicating a homogeneous prehistoric Rapa Nui population. Unfortunately, none of the prior Rapa Nui tribal analyses utilized multivariate or discriminate function analyses and only used univariate analyses, so a direct comparison of the results of this study to those could not be accomplished.

The minimum F_{ST} values, which are a minimum estimation of the degree of similarity/dissimilarity of the regions within the total population, indicate greater similarity between the male regional populations than the females. This in turn would necessitate greater levels of male pre- or postmarital migration. The determinant ratios do indicate the existence of increased male mobility for the majority of the prehistoric Rapa Nui tribal regions (Table 5); however, only the Northeast region was significantly different. The North and West regions, inhabited by the *Miru* tribe (Métraux, 1940; Routledge, 1919), the "Royal" tribe suspected of practicing the most extreme endogamy, possess

large ratios as well. With these results in mind, a reexamination of the ethnographic literature is required.

The prehistoric Rapa Nui society was predominantly a patrilineal society (McCall, 1979), and practiced a patri-virilocal post-marital residence pattern. Métraux (1940) reported that there were no marriage restrictions among tribes, save those of the *tumu*. A *tumu* was a group of people of one tribe who stood in a special relation to people of another, into which a man might marry. It was unclear as to whether marriage was obligatory or only customary between the *tumu*. With regards to the *Miru*, a more interesting picture develops, for marriage restrictions were more rigid for the royal lineage, but not the "common" *Miru*.

Within the *Miru* tribe, Métraux (1940) documented 13 lineages, of which only the Honga lineage claims direct descent from the first king; only a representative of the Honga lineage could be king. It was probably expected that the king had to marry within his own tribe, but not his own lineage. Other men of the *Miru* were not restricted as to the lineage or tribe they married into. The status of the "ordinary" members of the *Miru* was probably no different from that in other tribes (Métraux, 1940). However, a tradition existed in which it was improper for a man of another group to marry a *Miru* woman. The *Miru* had *tumus*, tribes within which they could marry. It was reported to Métraux that the *tumus* of the *Miru* were the *Hamea* and *Raa* (lesser tribes of the North and West coast), the *Tupahotu* and *Ureohei* (tribes of Northeastern and Eastern Rapa Nui), and the *Marama* (tribe of South and Southwestern Rapa Nui) (Fig. 2). The *Miru* were obviously the most widely distributed of the major tribes, and the potential for extensive intertribal marriage was there.

These ethnographic accounts more closely correspond with the results obtained in this study. The results indicate a relatively homogeneous prehistoric Rapa Nui population, with sufficient gene flow to negate the effects of genetic drift and of inbreeding due to extreme endogamy. Though insignificant, the observed determinant ratios indicate that intertribal migration was occurring,

TABLE 3. Unbiased Mahalanobis generalized squared distances (D^2) values¹

		Unbiased Mahalanobis generalized squared distances (D^2)				
From region	(n)	N	NE	S	SW	W
Males						
N	12	—	0.067116	0.167786	0.290538	0.105053
NE	36	0.088484	—	0.183659	0.174014	0.068013
S	31	0.246236	0.283357	—	0.339815	0.053036
SW	23	0.258060	0.050714	0.278276	—	0.265169
W	19	0.094923	0.046009	0.099465	0.141733	—
Minimum $F_{ST} = 0.06378^2/0.05870^3$						
Females						
N	7	—	0.257301	0.285430	0.533614	0.438929
NE	27	0.322824	—	0.236139	0.102611	0.107981
S	22	0.334227	0.387430	—	0.286567	0.169475
SW	17	0.849946	0.158442	0.506310	—	0.118021
W	12	0.575463	0.140917	0.264103	0.175583	—
Minimum $F_{ST} = 0.09409^2/0.141260^3$						

¹ Upper triangle 11-variable discriminant function, lower triangle six-variable discriminant function.² Minimum F_{ST} from 11-variable discriminant function.³ Minimum F_{ST} from six-variable discriminant function.TABLE 4. Unbiased Mahalanobis generalized squared distances (D^2) F -values¹

From region	(n)	Unbiased Mahalanobis generalized squared distances (D^2) F -values				
		N	NE	S	SW	W
Males						
N	12	—	0.050	0.121	0.190	0.064
NE	36	0.127	—	0.254	0.203	0.070
S	31	0.340	0.753	—	0.373	0.052
SW	23	0.325	0.114	0.586	—	0.229
W	19	0.111	0.091	0.187	0.235	—
$F_{05[4,106]} = 2.469^2/F_{05[4,111]} = 2.462^3$						
Females						
N	7	—	0.114	0.121	0.210	0.154
NE	27	0.280	—	0.228	0.085	0.071
S	22	0.277	0.734	—	0.219	0.105
SW	17	0.658	0.258	0.759	—	0.066
W	12	0.398	0.183	0.320	0.193	—
$F_{05[4,70]} = 2.517^2/F_{05[4,75]} = 2.510^3$						

¹ Upper triangle 11-variable discriminant function D^2 F -values, lower triangle six-variable discriminant function D^2 F -values.² Critical F -value for 11-variable discriminant function D^2 F -values.³ Critical F -value for six-variable discriminant function D^2 F -values.

and that neither a patrilocal or matrilineal postmarital migration pattern predominated. The relatively smaller unbiased Mahalanobis D^2 values and minimum F_{ST} values indicate that the males may have been the most mobile. The results of these analyses indicate that intertribal marriages were occurring, even among the *Miru* tribe (Métraux, 1940; Routledge, 1919), with the direction and amount of migration having been dictated by tribal social and political structure.

The cranial and postcranial discrete traits which have been utilized to support the theory of tribal endogamy, particularly for the *Miru* tribe and the tribes of the North-east and South coast, either no longer support this theory or could support an alternative theory. A recent analysis of a more extensive sample of Rapa Nui cranial discrete and continuous traits by Chapman (1999) has revealed no regional patterning, a finding that has contradicted his previous research (Chapman, 1993; Chapman and Gill, 1993). As with craniometrics, the non-metric cranial traits of the prehistoric Rapa Nui indicate a homogeneous population. Métraux (1940) reported 13 lineages within the *Miru* tribe, and presumably each tribe also contained numerous lineages with varying levels of hierarchy. The “royal” Honga lineage of the *Miru* practiced restricted exogamy, a practice the ruling lineages of other tribes may have accepted. The studies of Zimple and Gill (1986) and Gill and Owsley (1993) may document the practice of “lineage” endogamy/restricted exogamy, not necessarily complete tribal endogamy. Additionally, Gill et al. (1983) commented that the burial caves and *ahu* burial chambers, from which they analyzed the postcranial discrete trait frequencies, were family burial places. The high frequencies of certain postcranial discrete traits within the regional samples may indicate that the samples utilized may be biased and only reflect a few

TABLE 5. Ratios of determinants from male and female variance/covariance matrices

Region	11-variable				Six-variable			
	Males (n)	Females (n)	$ C\delta / C\varphi $	Randomization probability	Males (n)	Females (n)	$ C\delta / C\varphi $	Randomization probability
North	12	7	N/A	N/A	12	7	6.83	0.785
Northeast	36	25	83.39	0.008	36	27	11.07	0.024
South	31	21	12.24	0.290	31	21	4.24	0.173
Southwest	23	17	7.86	0.520	23	17	0.29	0.929
West	19	12	19,722	0.194	19	12	4.54	0.417

N/A, unable to calculate value due to small female sample.



Fig. 2. Rapa Nui tribal boundaries (adapted from Routledge, 1919, p 222).

families and not the entire regional population. This biased sample could present a picture of tribal endogamy, when in fact only lineage endogamy is documented.

The tribes on prehistoric Rapa Nui are known to have occupied distinctly separate areas (McCoy, 1973; Métraux, 1940; Routledge, 1919), yet the differentiation of those tribes did not occur through the actions of cultural and genetic isolation. Sufficient gene flow, most probably via intertribal marriage, occurred to maintain homogeneity among

the Rapa Nui islanders. Lineage endogamy or restricted exogamy probably was practiced by the “royal” and/or “ruling” lineages of the tribes, but the practice as reflected in craniofacial metric variation does not appear to have been widespread within the tribes as a whole, or practiced for a sufficient period of time to produce tribal distinctiveness.

Despite the intriguing results, it should be noted that this study has limitations, one is the fact that some of the regional samples

are small and therefore may not be representative of the underlying populations. Another limitation is that there may be some unknown sampling and collection bias within the museum collections of Rapanui crania. Yet, one of the strengths of this study is the incorporation of ethnographic data in the attempt to understand and interpret Rapa Nui regional population differences from craniometric data, and to explain and reconcile the different conclusions obtained from cranial and postcranial discrete trait analyses and those utilizing craniometric data analyses. Future studies will attempt to discover missing data estimation methods that can be employed with small samples, and utilize both cranial metric and discrete trait data to obtain a more comprehensive picture of Rapa Nui regional population cranial variation.

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Appendix. Craniometric measurements

Maximum cranial length	Biauricular breadth
Nasion-occipital length	Minimum cranial breadth
Frontal chord	Auricular height
Parietal chord	Porion-bregma
Maximum cranial breadth	Porion-nasion
Biasterionic breadth	Porion-subnasale
Basion-bregma	Porion-prosthion
Basion-nasion	Maxillofrontal breadth
Basion-prosthion	Maxillofrontal subtense
Basion-porion	Zygoorbital breadth
Bistephanic breadth	Zygoorbital subtense
Maximum frontal breadth	Alpha chord
Minimum frontal breadth	Alpha subtense
Bijugal breadth	Simotic chord
Bizygomatic breadth	Bimaxillary breadth
Nasion-prosthion	Bimaxillary subtense
Maxillary length	Mastoid length
Maxillary breadth	Mastoid breadth
Palatal depth	Cheek height
Nasal height	Malar length, inferior
Nasal breadth	Malar length, maximum
Left orbital height	Foramen magnum length
Left orbital breadth-dacryon	Nasion-alveolare
Biorbital breadth	Nasion-gnathion
Bifrontal breadth	Left orbital breadth, maxillofrontale

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